

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 05:40:06 ; Search time 1838.32 Seconds
(without alignments)
12203.124 Million cell updates/sec

Title: US-09-811-118-2

Perfect score: 1072
Sequence: 1 GAGCGCGCCACCTCCGGAAC.....TTGCATCCACATGATTTTC 1072

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hgt:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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23: em_pat:*
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29: em_vl:*
30: em_hgt_hum:*
31: em_hgt_inv:*
32: em_hgt_other:*
33: em_hgt_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Query Length | DB ID | Description |
|------------|-------------|--------------|-------|-------------|
|------------|-------------|--------------|-------|-------------|

| | | | | | | |
|----|------|-------|--------|----|-----------|---------------------|
| 1 | 1072 | 100.0 | 1072 | 6 | AR151077 | AR151077 Sequence |
| 2 | 921 | 85.9 | 1511 | 6 | AX188360 | AX188360 Sequence |
| 3 | 919 | 85.7 | 1228 | 9 | AK027683 | AK027683 Homo sapi |
| 4 | 916 | 85.4 | 1227 | 6 | AX080813 | AX080813 Sequence |
| 5 | 667 | 62.2 | 857 | 9 | AF091092 | AF091092 Homo sapi |
| 6 | 629 | 58.7 | 1251 | 6 | AX080809 | AX080809 Sequence |
| 7 | 596 | 55.6 | 160066 | 2 | AL356976 | AL356976 Homo sapi |
| 8 | 361 | 33.7 | 751 | 6 | AX186595 | AX186595 Sequence |
| 9 | 356 | 33.2 | 468 | 6 | AX187668 | AX187668 Sequence |
| 10 | 151 | 14.1 | 51381 | 2 | AF322456 | AF322456 Homo sapi |
| 11 | 80 | 7.5 | 51381 | 2 | AF322456 | AF322456 Homo sapi |
| 12 | 79 | 7.4 | 55891 | 2 | AC022847 | AC022847 Homo sapi |
| 13 | 50 | 4.7 | 50 | 6 | AX080812 | AX080812 Sequence |
| 14 | 49 | 4.6 | 1033 | 10 | BC003228 | BC003228 Mus muscu |
| 15 | 46 | 4.3 | 241048 | 2 | AL627238 | AL627238 Mus muscu |
| 16 | 44 | 4.1 | 164683 | 2 | AC097883 | AC097883 Rattus no |
| 17 | 27 | 2.5 | 100000 | 9 | AP000077 | AP000077 Homo sapi |
| 18 | 27 | 2.5 | 100414 | 9 | AC011596 | AC011596 Homo sapi |
| 19 | 27 | 2.5 | 158523 | 2 | AC013547 | AC013547 Homo sapi |
| 20 | 27 | 2.5 | 166009 | 2 | AC011061 | AC011061 Homo sapi |
| 21 | 26 | 2.4 | 164683 | 2 | AC097883 | AC097883 Rattus no |
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| 24 | 25 | 2.3 | 201408 | 9 | AC090644 | AC090644 Homo sapi |
| 25 | 24 | 2.2 | 24 | 6 | AX080810 | AX080810 Sequence |
| 26 | 24 | 2.2 | 24 | 6 | AX080811 | AX080811 Sequence |
| 27 | 24 | 2.2 | 140781 | 2 | AC008611 | AC008611 Homo sapi |
| 28 | 24 | 2.2 | 141513 | 9 | AC020905 | AC020905 Homo sapi |
| 29 | 24 | 2.2 | 164468 | 2 | AC021899 | AC021899 Homo sapi |
| 30 | 24 | 2.2 | 165201 | 2 | AC090597 | AC090597 Homo sapi |
| 31 | 24 | 2.2 | 165943 | 2 | AC022205 | AC022205 Homo sapi |
| 32 | 24 | 2.2 | 166518 | 9 | AC090514 | AC090514 Homo sapi |
| 33 | 24 | 2.2 | 193424 | 4 | AC005690 | AC005690 Homo sapi |
| 34 | 24 | 2.2 | 197836 | 4 | AC090032 | AC090032 Canis fam |
| 35 | 24 | 2.2 | 197901 | 2 | AC018621 | AC018621 Homo sapi |
| 36 | 24 | 2.2 | 200204 | 9 | AC018626 | AC018626 Homo sapi |
| 37 | 24 | 2.2 | 205416 | 2 | AC107388 | AC107388 Homo sapi |
| 38 | 24 | 2.2 | 20767 | 2 | AP001497 | AP001497 Homo sapi |
| 39 | 23 | 2.1 | 767 | 10 | AF045769 | AF045769 Mus muscu |
| 40 | 23 | 2.1 | 876 | 10 | AF045768 | AF045768 Mus muscu |
| 41 | 23 | 2.1 | 958 | 10 | D87896 | D87896 Mus muscu |
| 42 | 23 | 2.1 | 989 | 10 | AF274027 | AF274027 Mus muscu |
| 43 | 23 | 2.1 | 1380 | 10 | AF044056 | AF044056 Mus muscu |
| 44 | 23 | 2.1 | 2075 | 10 | MM0291744 | MM0291744 Mus muscu |
| 45 | 23 | 2.1 | 3980 | 10 | MM0212104 | MM0212104 Mus muscu |

ALIGNMENTS

| | | | | | | |
|-----------------------|--|---------------------------|---------|-------|--------|-----------------|
| RESULT 1 | AR151077 | AR151077 | 1072 bp | DNA | linear | PAT 08-AUG-2001 |
| LOCUS | Sequence | 2 from patent US 6231853. | | | | |
| DEFINITION | AR151077 | | | | | |
| ACCESSION | AR151077.1 | GI:15117127 | | | | |
| VERSION | | | | | | |
| KEYWORDS | Unknown. | | | | | |
| SOURCE | Unknown. | | | | | |
| ORGANISM | Unclassified. | | | | | |
| REFERENCE | 1 (bases 1 to 1072) | | | | | |
| AUTHORS | Hillman,J.L., Corley,N.C. and Patterson,C. | | | | | |
| TITLE | Human glutathione peroxidase-6 | | | | | |
| JOURNAL | Patent: US 6231853-A 2 15-MAY-2001; | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
| source | 1..1072 | | | | | |
| BASE COUNT | 275 a | 294 c | 270 g | 233 t | | |
| ORIGIN | /organism="unknown" | | | | | |
| Query Match | 100.0%; | Score | 1072; | DB | 6; | Length 1072; |
| Best Local Similarity | 100.0%; | Pred. | No. 0; | | | |

| Matches 1072; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
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| QY | 1 | GAGCCGCCACCTCCGGAACAGCAGATGTCGGCGGCGAGCGGTGCGACGGCGGTGCTGCT | 60 | | | | | | |
| Db | 1 | GAGCCGCCACCTCCGGAACAGCAGATGTCGGCGGCGAGCGGTGCGACGGCGGTGCTGCT | 60 | | | | | | |
| QY | 61 | CTGTGGGCTGCGGCTGCGCGAGCAGCAGAGCAGACTTCTAGACTTCAAGCGGTCAA | 120 | | | | | | |
| Db | 61 | CTGTGGGCTGCGGCTGCGCGAGCAGCAGAGCAGACTTCTAGACTTCAAGCGGTCAA | 120 | | | | | | |
| QY | 121 | CATCCGGGGCAAACTGTGTGCTGCTGGAGAGTACCGGGGATCGGTGTCCTGGGTGGAA | 180 | | | | | | |
| Db | 121 | CATCCGGGGCAAACTGTGTGCTGCTGGAGAGTACCGGGGATCGGTGTCCTGGGTGGAA | 180 | | | | | | |
| QY | 181 | TGTGGCCAGGAGTGCAGCTTACAGACAGCAGACTACGAGCCCTGAGCAGCTGACGC | 240 | | | | | | |
| Db | 181 | TGTGGCCAGGAGTGCAGCTTACAGACAGCAGACTACGAGCCCTGAGCAGCTGACGC | 240 | | | | | | |
| QY | 241 | AGACCTGGGCCCCCACCACCTTCAACGCTGCTGCTTCCCTGCAACAGTTGGCCAA | 300 | | | | | | |
| Db | 241 | AGACCTGGGCCCCCACCACCTTCAACGCTGCTGCTTCCCTGCAACAGTTGGCCAA | 300 | | | | | | |
| QY | 301 | GGAAGCTGACAGCAACAGAGATTTGAGAGCTTTCCTGCGGCACTACAGTGTCTCAT | 360 | | | | | | |
| Db | 301 | GGAAGCTGACAGCAACAGAGATTTGAGAGCTTTCCTGCGGCACTACAGTGTCTCAT | 360 | | | | | | |
| QY | 361 | CCCCATGTTAGCAAGATTCAGTCAACGGTACTGTGTCCTGCTGCTGCTGCTGCT | 420 | | | | | | |
| Db | 361 | CCCCATGTTAGCAAGATTCAGTCAACGGTACTGTGTCCTGCTGCTGCTGCTGCT | 420 | | | | | | |
| QY | 421 | GGCCCAACTTCTGGGAAAGAGCCCACTGTAAGTGTGTAAGTACTAGTACGCCCA | 480 | | | | | | |
| Db | 421 | GGCCCAACTTCTGGGAAAGAGCCCACTGTAAGTGTGTAAGTACTAGTACGCCCA | 480 | | | | | | |
| QY | 481 | TGGAAGGTGTGGAGGCTTGGGACCCCACTGTCAGTGGAGAGGTGACACTCCAGAT | 540 | | | | | | |
| Db | 481 | TGGAAGGTGTGGAGGCTTGGGACCCCACTGTCAGTGGAGAGGTGACACTCCAGAT | 540 | | | | | | |
| QY | 541 | CACAGCGCTGTGAGAGAGCTCATCTAGTAAGCGAAGAGCTTATPACCACCGGCT | 600 | | | | | | |
| Db | 541 | CACAGCGCTGTGAGAGAGCTCATCTAGTAAGCGAAGAGCTTATPACCACCGGCT | 600 | | | | | | |
| QY | 601 | CTCTCTCACACCTCATCCCGCCACCTGTGTGGGCTGACCAATCCAACTCAATAG | 660 | | | | | | |
| Db | 601 | CTCTCTCACACCTCATCCCGCCACCTGTGTGGGCTGACCAATCCAACTCAATAG | 660 | | | | | | |
| QY | 661 | TGCTTAAAGGAGAGAGCCCACTGCTCTCTCTTACTCTTATGCAATGCTGCTCCAT | 720 | | | | | | |
| Db | 661 | TGCTTAAAGGAGAGAGCCCACTGCTCTCTCTTACTCTTATGCAATGCTGCTCCAT | 720 | | | | | | |
| QY | 721 | CATTCTTGTGGGGAAAAATTTCTAGTATTTTGTATTTTGAATCTTACAGCAACAAAT | 780 | | | | | | |
| Db | 721 | CATTCTTGTGGGGAAAAATTTCTAGTATTTTGTATTTTGAATCTTACAGCAACAAAT | 780 | | | | | | |
| QY | 781 | GAACTCTGCGCATATGAGAGCTTGTGACAGTGAATCACCAGCCGATACAGAGCTTTC | 840 | | | | | | |
| Db | 781 | GAACTCTGCGCATATGAGAGCTTGTGACAGTGAATCACCAGCCGATACAGAGCTTTC | 840 | | | | | | |
| QY | 841 | CAACAAAAATGTGTGCAATATAGATATATCAAGCAATATCTCCACCAAGGCTTCT | 900 | | | | | | |
| Db | 841 | CAACAAAAATGTGTGCAATATAGATATATCAAGCAATATCTCCACCAAGGCTTCT | 900 | | | | | | |
| QY | 901 | GTAAGTGGAGCAATGATTACCTCATAGGGCTGTTGTGAGGATTTAGATGAATACCT | 960 | | | | | | |
| Db | 901 | GTAAGTGGAGCAATGATTACCTCATAGGGCTGTTGTGAGGATTTAGATGAATACCT | 960 | | | | | | |
| QY | 961 | TGAAAGTCTTAGGAGTGCAGCAATATAGAGGCAATTAATGATGATATTTTTCATAT | 1020 | | | | | | |
| Db | 961 | TGAAAGTCTTAGGAGTGCAGCAATATAGAGGCAATTAATGATGATATTTTTCATAT | 1020 | | | | | | |
| QY | 1021 | AAACCAAAAAATATCTTATCAATAAAGTTCATCAACATGAAATTC | 1072 | | | | | | |
| Db | 1021 | AAACCAAAAAATATCTTATCAATAAAGTTCATCAACATGAAATTC | 1072 | | | | | | |

| Query Match 85.9%; Score 921; DB 6; Length 1511; Best Local Similarity 99.8%; Pred. No. 0; Matches 1021; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | | | | | | | | | |
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| QY | 1 | GAGCCGCCACCTCCGGAACAGCAGATGTCGGCGGCGAGCGGTGCGACGGCGGTGCTGCT | 60 | | | | | | |
| Db | 276 | GAGCCGCCACCTCCGGAACAGCAGATGTCGGCGGCGAGCGGTGCGACGGCGGTGCTGCT | 335 | | | | | | |
| QY | 61 | CTGTGGGCTGCGGCTGCGCGAGCAGCAGAGCAGACTTCTAGACTTCAAGCGGTCAA | 120 | | | | | | |
| Db | 336 | CTGTGGGCTGCGGCTGCGCGAGCAGCAGAGCAGACTTCTAGACTTCAAGCGGTCAA | 395 | | | | | | |
| QY | 121 | CATCCGGGGCAAACTGTGTGCTGCTGGAGAGTACCGGGATCGGTGTCCTGGGTGGAA | 180 | | | | | | |
| Db | 396 | CATCCGGGGCAAACTGTGTGCTGCTGGAGAGTACCGGGATCGGTGTCCTGGGTGGAA | 455 | | | | | | |
| QY | 181 | TGTGGCCAGGAGTGCAGCTTACAGACAGCAGACTACGAGCCCTGAGCAGCTGACGC | 240 | | | | | | |
| Db | 456 | TGTGGCCAGGAGTGCAGCTTACAGACAGCAGACTACGAGCCCTGAGCAGCTGACGC | 515 | | | | | | |
| QY | 241 | AGACCTGGGCCCCCACCACCTTCAACGCTGCTGCTTCCCTGCAACAGTTGGCCAA | 300 | | | | | | |
| Db | 516 | AGACCTGGGCCCCCACCACCTTCAACGCTGCTGCTTCCCTGCAACAGTTGGCCAA | 575 | | | | | | |
| QY | 301 | GGAAGCTGACAGCAACAGAGATTTGAGAGCTTTCCTGCGGCACTACAGTGTCTCAT | 360 | | | | | | |
| Db | 576 | GGAAGCTGACAGCAACAGAGATTTGAGAGCTTTCCTGCGGCACTACAGTGTCTCAT | 635 | | | | | | |
| QY | 361 | CCCCATGTTAGCAAGATTCAGTCAACGGTACTGTGTCCTGCTGCTGCTGCTGCT | 420 | | | | | | |
| Db | 636 | CCCCATGTTAGCAAGATTCAGTCAACGGTACTGTGTCCTGCTGCTGCTGCTGCT | 695 | | | | | | |
| QY | 421 | GGCCCAACTTCTGGGAAAGAGCCCACTGTAAGTGTGTAAGTACTAGTACGCCCA | 480 | | | | | | |
| Db | 696 | GGCCCAACTTCTGGGAAAGAGCCCACTGTAAGTGTGTAAGTACTAGTACGCCCA | 755 | | | | | | |
| QY | 481 | TGGAAGGTGTGGAGGCTTGGGACCCCACTGTCAGTGGAGAGGTGAGACTTCCAGAT | 540 | | | | | | |
| Db | 756 | TGGAAGGTGTGGAGGCTTGGGACCCCACTGTCAGTGGAGAGGTGAGACTTCCAGAT | 815 | | | | | | |
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| Db | 816 | CACAGCGCTGTGAGAGTGCAGCAATATAGAGGCAATTAATGATGATATTTTTCATAT | 875 | | | | | | |
| QY | 601 | CTCTCTCACACCTCATCCCGCCACCTGTGTGGGCTGACCAATGCAACTCAATAG | 660 | | | | | | |

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Db 936 TCGTCAAGAGGAGAGACCCACTGCTCTCTCTTACTCTTATGCAATGGTCCAT 995
QY 721 CATCTCTGGGGGAAAAATTTCTAGTATTTTGAATTTTGAATCTTACAGCAACAATAG 780
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QY 781 GAACCTCTGGGCAATGAGAGCTTGTACCAATGCAATGCAATGCAATGCAATG 840
Db 1056 GAACCTCTGGGCAATGAGAGCTTGTACCAATGCAATGCAATGCAATGCAATG 1115
QY 841 CAACAAAAATGTGTGCAATGAGTATATCAAGCAATATCTCCACCAAGGCTCT 900
Db 1116 CAACAAAAATGTGTGCAATGAGTATATCAAGCAATATCTCCACCAAGGCTCT 1175
QY 901 GTAACTGGGACCAATGATTACTCTAGGCTGTGTGAGATTTAGATGAATACCTG 960
Db 1176 GTAACTGGGACCAATGATTACTCTAGGCTGTGTGAGATTTAGATGAATACCTG 1235
QY 961 TGAAGTGGCTTGGAGCTGCTCCAGCCCAATAGAGAGCATTCATGAACATTTTTCATAT 1020
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QY 1021 AAA 1023
Db 1296 AAA 1298

RESULT 3
AK027683 1228 bp mRNA linear PRI 15-MAY-2001
LOCUS AK027683
DEFINITION Homo sapiens CDNA FLJ14777 fis, clone NT2RP4000259, weakly similar
to GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).
ACCESSION AK027683
VERSION AK027683.1 GI:14042545
KEYWORDS oligo cloning; fis (full insert sequence).
SOURCE Homo sapiens testicular carcinoma cell line:NT2 CDNA to mRNA,
clone_11b:NT2RP4 clone:NT2RP4000259.

ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (sites)
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Aotsuka,S., Yoshikawa,Y.,
Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,U.,
Wakamatsu,A., Nakamura,Y., Negahari,K., Masuho,Y. and Sasaki,N.
TITLE NEDD human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1228)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEDD human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction;
5'- & 3'-end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES
source Location/Qualifiers

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BASE COUNT 326 a 330 c 290 g 282 t
ORIGIN

Query Match 85.7%; Score 919; DB 9; Length 1228;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 4
AX080813 1227 bp DNA linear PAT 27-FEB-2001
LOCUS Sequence 59 from Patent WO0109327.
DEFINITION AX080813
ACCESSION AX080813.1 GI:13169783
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1227)
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,
Kljasvin, I.J., Lafleur, M., Mark, M.R., Masters, S.A., Pitt, R.M.,
Watanabe, C.K. and Wood, W.I.
TITLE Method of preventing the injury or death of retinal cells and
treating ocular diseases
JOURNAL Patent: WO 0109327-A 59 08-FEB-2001;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
source 1..1227
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 331 a 325 c 293 g 278 t
ORIGIN

Query Match 85.4%; Score 916; DB 6; Length 1227;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1066; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCGCCACCTCCGGAACAAGCCATGTTGGCGGAGCGTGCGGCGCTGCTCTCT 63
Db 12 GCCGCCACCTCCGGAACAAGCCATGTTGGCGGAGCGTGCGGCGCTGCTCTCT 71
QY 64 GTGGGCTGGGCGCTGGCGGAGAGAGAGAGCTTCTACGATTTCAAGCGGTCAACAT 123
Db 72 GTGGGCTGGGCGCTGGCGGAGAGAGAGAGAGCTTCTACGATTTCAAGCGGTCAACAT 131
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QY 304 GCGTGACAGCAACAGAGAGATTGAGAGCTTTGCGCGGACCTACAGTGTCTCATTTCC 363
Db 312 GCGTGACAGCAACAGAGAGATTGAGAGCTTTGCGCGGACCTACAGTGTCTCATTTCC 371

QY 364 CATGTTAGCAAGATTGCAATACCGGTACTGTGCGCCATCTGCTTCAAGTACTGGC 423
Db 372 CATGTTAGCAAGATTGCAATACCGGTACTGTGCGCCATCTGCTTCAAGTACTGGC 431
QY 424 CCAGACTTCTGGGAGAGAGAGCCACCTGGAACCTTGTGAAGTACTGATAGCCCCAGATG 483
Db 432 CCAGACTTCTGGGAGAGAGAGCCACCTGGAACCTTGTGAAGTACTGATAGCCCCAGATG 491
QY 484 AAGGTGTAGAGGGCTTGGGAGCCACTGTGTAGTGGAGAGGTGACATCCAGATCAC 543
Db 492 AAGGTGTAGAGGGCTTGGGAGCCACTGTGTAGTGGAGAGGTGACATCCAGATCAC 551
QY 544 AGCGCTGTGAGAGAGAGCCACTGTGTAGTGGAGAGAGGTGACATCCAGATCAC 603
Db 552 AGCGCTGTGAGAGAGAGCCACTGTGTAGTGGAGAGAGGTGACATCCAGATCAC 611
QY 604 CCGTCCACACCTCATCTCCCGCCACCTGTGTGGGCGCTGACCAATGCAAACTCAATGTGCG 663
Db 612 CCGTCCACACCTCATCTCCCGCCACCTGTGTGGGCGCTGACCAATGCAAACTCAATGTGCG 671
QY 664 TTCAAGAGGAGAGAGCCACTGTGTAGTGGAGAGAGGTGACATCCAGATCAC 723
Db 672 TTCAAGAGGAGAGAGCCACTGTGTAGTGGAGAGAGGTGACATCCAGATCAC 731
QY 724 TCTTGTGGGGGAAAAATTTAGTATTTTGAATTTTGAATCTTACAGCAACAATAGGAA 783
Db 732 TCTTGTGGGGGAAAAATTTAGTATTTTGAATTTTGAATCTTACAGCAACAATAGGAA 791
QY 784 CTCTGTGGCAATAGAGCTTGTACCAAGTGAATCACCAGCCGATACGAAGCTTTCGCA 843
Db 792 CTCTGTGGCAATAGAGCTTGTACCAAGTGAATCACCAGCCGATACGAAGCTTTCGCA 851
QY 844 CAATAATGTGTGCAATATAGATATATCAAGCAATATCTCCACCAAGGCTTCTGTA 903
Db 852 CAATAATGTGTGCAATATAGATATATCAAGCAATATCTCCACCAAGGCTTCTGTA 911
QY 904 AACTGGAGCCATGATTACCTCATAGGGCTGTTGTAGAGATTAGATGAATATCTGTGA 963
Db 912 AACTGGAGCCATGATTACCTCATAGGGCTGTTGTAGAGATTAGATGAATATCTGTGA 971
QY 964 AAGTGGCTAGGAGCTGCGACCAATATAGAGAGATTCATGAACATTTTTCATATAA 1023
Db 972 AAGTGGCTAGGAGCTGCGACCAATATAGAGAGATTCATGAACATTTTTCATATAA 1031
QY 1024 CCAAAAAATTAATCTGTTATCAATAAAACTTGATCCACATGAATTTTC 1072
Db 1032 CCAAAAAATTAATCTGTTATCAATAAAACTTGATCCACATGAATTTTC 1080

RESULT 5
AF091092 857 bp mRNA linear PRI 12-NOV-1998
LOCUS Homo sapiens clone 683 unknown mRNA, complete sequence.
DEFINITION AF091092
ACCESSION AF091092.1 GI:3860021
VERSION
KEYWORDS FLI_CDNA.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 857)
AUTHORS Barrow, I.K.-P., Boguski, M.S., Touchman, J., and Spencer, F.
TITLE Full-insert sequence of mapped XREF EST
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 857)
AUTHORS Barrow, I.K.-P., Boguski, M.S., Touchman, J., and Spencer, F.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-1998) NHGRI, NIH, 49 Convent Drive, Building 49,
Room 2C08, Bethesda, MD 20892, USA
FEATURES
source 1..857
/organism="Homo sapiens"

/db_xref="taxon:9606"
 /chromosome="1"
 /map="1q24-q41"
 /clone="683"
 /note="location inferred using conservation of syntenly
 with mouse locus D1Xt379"
 46..225
 CDS

/note="similar to Saccharomyces cerevisiae ORF YBR244W"
 /product="start=1"
 /codon_start=1
 /protein_id="AAC72961.1"
 /db_xref="GI:3860022"
 /translation="MANSLTATRLRLALPAAPVSHSPCLARLOSPLYLPSSTW
 PLLLRSPPTSGST"

BASE COUNT 267 a 216 c 184 g 190 t
 ORIGIN

Query Match 62.2%; Score 667; DB 9; Length 857;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 767; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 255 ACCACTTCACGTCGCGCTTCCCTGCAACAGATTGGCCAAAGAGAGCTGACAGCA 314
 DB 10 ACCACTTCACGTCGCGCTTCCCTGCAACAGATTGGCCAAAGAGAGCTGACAGCA 69
 QY 315 ACAAGAGATTGAGAGCTTGCCTGCCGACACTACAGTGTCTCATTCCTCCATGTTAGCA 374
 DB 70 ACAAGAGATTGAGAGCTTGCCTGCCGACACTACAGTGTCTCATTCCTCCATGTTAGCA 129
 QY 375 ACATTGCACTACACGGTACTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 434
 DB 130 ACATTGCACTACACGGTACTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 189
 QY 435 GGAGAGGCCACCGTGGAGCTTCTGGAAGTACCTAGACCCAGATGGAAGAGTGTGAG 494
 DB 190 GGAGAGGCCACCGTGGAGCTTCTGGAAGTACCTAGACCCAGATGGAAGAGTGTGAG 249
 QY 495 GGGCTTGGAGCCCACTGTGTGTCAGTGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 554
 DB 250 GGGCTTGGAGCCCACTGTGTGTCAGTGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 309
 QY 555 GGAAGTCTACTCTACTGAAAGCAAGACTTATACACCGGCTGCTGCTGCTGCTGCTGCTG 614
 DB 310 GGAAGTCTACTCTACTGAAAGCAAGACTTATACACCGGCTGCTGCTGCTGCTGCTGCTG 369
 QY 615 TCATCCCGCCACCGTGTGGGGCTGACCAATGCAAACTGATGCTGCTGCTGCTGCTGCTG 674
 DB 370 TCATCCCGCCACCGTGTGGGGCTGACCAATGCAAACTGATGCTGCTGCTGCTGCTGCTG 429
 QY 675 AGACCCACTGACTCTGCTGCTTACTCTTATGTCATGCTGCTGCTGCTGCTGCTGCTGCTG 734
 DB 430 AGACCCACTGACTCTGCTGCTTACTCTTATGTCATGCTGCTGCTGCTGCTGCTGCTGCTG 489
 QY 735 AAAAATTCTAGATTGTTGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 794
 DB 490 AAAAATTCTAGATTGTTGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 549
 QY 795 TGAGAGCTCTGTCAGTGAATGACAGCGAGTAGAGAGTCTGTCACCAAAAGTGTGT 854
 DB 550 TGAGAGCTCTGTCAGTGAATGACAGCGAGTAGAGAGTCTGTCACCAAAAGTGTGT 609
 QY 855 GGCAGAAATAGATATATCAAGCAATATCTCCACCAAGGCTTCTGTAACAGTGGAGCA 914
 DB 610 GGCAGAAATAGATATATCAAGCAATATCTCCACCAAGGCTTCTGTAACAGTGGAGCA 659
 QY 915 ATGATTACTCATAGGCTGTGTGTGAGATTAGATGAATATACCTGTGAAAGTGGCTAGG 974
 DB 670 ATGATTACTCATAGGCTGTGTGTGAGATTAGATGAATATACCTGTGAAAGTGGCTAGG 729
 QY 975 CAGTGCAGCAAAATAGAGGAGCATTCATGAATATTTTGGCATATATAA 1023
 DB 730 CAGTGCAGCAAAATAGAGGAGCATTCATGAATATTTTGGCATATATAA 778

RESULT 6
 AX080809
 LOCUS AX080809 1251 bp DNA linear PAT 27-FEB-2001

DEFINITION Sequence 55 from Patent WO0109327.
 AX080809
 ACCESSION AX080809
 VERSION AX080809.1 GI:13169779

KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 1 (bases 1 to 1251)
 Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,
 Kljavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,
 Matanabe, C.K. and Wood, W.I.
 Method of preventing the injury or death of retinal cells and
 treating ocular diseases
 Patent: WO 0109327-A 55 08-FEB-2001;
 Genentech, Inc. (US)

TITLE
 JOURNAL
 FEATURES

source
 location/Qualifiers
 1..1251
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Partial DNA sequence used to isolate DNA57037."

unsure
 BASE COUNT 343 a 328 c 298 g 280 t 2 others
 ORIGIN

Query Match 58.7%; Score 629; DB 6; Length 1251;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 GGTGCCATCTCTGCTTCAAGTACCTGCGCCAGACTTCTGGAGAGAGCCACCTGGAAC 454
 DB 401 GGTGCCATCTCTGCTTCAAGTACCTGCGCCAGACTTCTGGAGAGAGCCACCTGGAAC 460
 QY 455 TTCTGGAAGTACTAGTACGCCCGAGATGGAAGTGTGGGGCTTGGAGCCCACTGTG 514
 DB 461 TTCTGGAAGTACTAGTACGCCCGAGATGGAAGTGTGGGGCTTGGAGCCCACTGTG 520
 QY 515 TCAGTGGAGAGGTGCACTCCAGATCAGAGCGCTGCTGAGAGAGTCACTCTACTGAG 574
 DB 521 TCAGTGGAGAGGTGCACTCCAGATCAGAGCGCTGCTGAGAGAGTCACTCTACTGAG 580
 QY 575 CGAGAGACTTATTAACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
 DB 581 CGAGAGACTTATTAACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 640
 QY 635 GGGCTGACCAATGCAAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 694
 DB 641 GGGCTGACCAATGCAAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 700
 QY 695 CTTTACTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 754
 DB 701 CTTTACTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 760
 QY 755 TATTTGAATCTTACAGCAAAATAGAGACTCTGSCCAATGAGAGCTTGTGACAGTGA 814
 DB 761 TATTTGAATCTTACAGCAAAATAGAGACTCTGSCCAATGAGAGCTTGTGACAGTGA 820
 QY 815 ATACAGCGCGATAGAGAGTCTGTCACCAAAAGTGTGCGAAATAGAGATATTCGA 874
 DB 821 ATACAGCGCGATAGAGAGTCTGTCACCAAAAGTGTGCGAAATAGAGATATTCGA 880
 QY 875 GCAATATCTCCACCCCAAGGCTTCTGTAACAGTGGAGCAATGATTACTCATAGGGCTG 934
 DB 881 GCAATATCTCCACCCCAAGGCTTCTGTAACAGTGGAGCAATGATTACTCATAGGGCTG 940
 QY 935 TTGTGAGATTAGATGAATATACCTGTGAAAGTGGCTAGGAGTGCAGCAATATAGAG 994

Db 941 TTGTGAGATTAGCATGAATACCTGTGAAGTGCCTAGCAGCTGCCAGCCAAATAGAG 1000
OY 995 GCATTCATGACATTTTTCATATATA 1023
Db 1001 GCATTCATGACATTTTTCATATATA 1029

RESULT 7
AL356976 160066 bp DNA linear HTG 08-FEB-2002
LOCUS Homo sapiens chromosome 1 clone RP4-700P11 map p32.1-32.3, ***
DEFINITION SEQUENCING IN PROGRESS ***, 5 unordered pieces.
ACCESSION AL356976
VERSION AL356976.18 GI:18643752
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Van Hellmond, Z.
Direct Submission
Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 10, 2002 this sequence version replaced gi:18477299.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
Project Information
Center project name: dj700P11
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 6% of reads
Dye-terminator Big Dye; 93% of reads
Consensus quality: 157881 bases at least Q40
Consensus quality: 158054 bases at least Q30
Consensus quality: 159095 bases at least Q20
Insert size: 159666; sum-of-contrigs
Insert size: 111224; 66.8% error; agarose-fp
Quality coverage: 7.58% in Q20 bases; sum-of-contrigs Quality
coverage: 12.72% in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 87143: contrig of 87143 bp in length
* 87144 87243: gap of 100 bp
* 87244 94440: contrig of 7197 bp in length
* 94441 94540: gap of 100 bp
* 94541 117956: contrig of 23416 bp in length
* 117957 118056: gap of 100 bp
* 118057 157663: contrig of 39607 bp in length
* 157664 157763: gap of 100 bp
* 157764 160066: contrig of 2303 bp in length.
Location/Qualifiers
1. 160066
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="p32.1-32.3"
/clone="RP4-700P11"
/clone.lib="RPCI-4"
1. 87143
misc_feature
/note="assembly_fragment:01501"

misc_feature
87244..94440
/note="assembly_fragment:00811
fragment_chain:1"
misc_feature
94541..117956
/note="assembly_fragment:02643
fragment_chain:1"
118057..157663
/note="assembly_fragment:03016
fragment_chain:1"
misc_feature
157764..160066
/note="assembly_fragment:01821"
BASE COUNT 42972 a 35602 c 36676 g 44415 t 401 others
ORIGIN

Query Match 55.6%; Score 596; DB 2; Length 160066;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 426 AGACTCTGGGAGAGAGCCACCTGAGACTCTGAGAGTACCTAGTACGAGATGAA 485
|||||
Db 112388 AGACTCTGGGAGAGAGCCACCTGAGACTCTGAGAGTACCTAGTACGAGATGAA 112329
OY 486 AGCTGTAGAGGCGCTTGGAGCCCACTGTGTCACTGTGAGGAGGTCACATCCAGATCACAG 545
|||||
Db 112328 AGCTGTAGAGGCGCTTGGAGCCCACTGTGTCACTGTGAGGAGGTCACATCCAGATCACAG 112269
OY 546 CGCTGTGAGAGAGTCTATCTTCTGATGAGAGGAGAGAGTATTAACCGCGCTCTCTCC 605
|||||
Db 112268 CGCTGTGAGAGAGTCTATCTTCTGATGAGAGGAGAGAGTATTAACCGCGCTCTCTCC 112209
OY 606 TCACACACCTCATCCGCCACCTGTGTGGGGTGCACATGCAATCAATGGTCTT 665
|||||
Db 112208 TCACACACCTCATCCGCCACCTGTGTGGGGTGCACATGCAATCAATGGTCTT 112149
OY 666 CAAAGGAGAGAGAGCCACCTGCTCTCTTACTCTTATGCAATGGTCTCCATCTTC 725
|||||
Db 112148 CAAAGGAGAGAGAGCCACCTGCTCTCTTACTCTTATGCAATGGTCTCCATCTTC 112089
OY 726 TTGTGGGGGAAAAATCTGTATTTTGTATTTTGAATCTTACAGCAAAATAGAACT 785
|||||
Db 112088 TTGTGGGGGAAAAATCTGTATTTTGTATTTTGAATCTTACAGCAAAATAGAACT 112029
OY 786 CTTGGCCAAATGAGAGCTCTTGACAGTATCACAGCCGATACGAGCTTTGCCAACA 845
|||||
Db 112028 CTTGGCCAAATGAGAGCTCTTGACAGTATCACAGCCGATACGAGCTTTGCCAACA 111969
OY 846 AAAATGTGTGGCAATAGAGATATCAAGCAATATCTCCACCCAGAGCTTGTGTAA 905
|||||
Db 111968 AAAATGTGTGGCAATAGAGATATCAAGCAATATCTCCACCCAGAGCTTGTGTAA 111909
OY 906 CTGGGACCAATGATTTACCTATAGGCGCTGTGTGAGAGTTAGATGCAATACCTGTGAA 965
|||||
Db 111908 CTGGGACCAATGATTTACCTATAGGCGCTGTGTGAGAGTTAGATGCAATACCTGTGAA 111849
OY 966 GTGCTTAGCAGAGTGCAGCAAAATAGAGAGATCAATGAACATTTTTCATATTAAC 1025
|||||
Db 111848 GTGCTTAGCAGAGTGCAGCAAAATAGAGAGATCAATGAACATTTTTCATATTAAC 111789
OY 1026 AAAAAATTAATCTGTATCAATATAAAACCTTGATCAATCAATGATTTTC 1072
|||||
Db 111788 AAAAAATTAATCTGTATCAATATAAAACCTTGATCAATCAATGATTTTC 111742

RESULT 8
AX186595
LOCUS AX186595/C 751 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 2290 from Patent WO0142467.
ACCESSION AX186595
VERSION AX186595.1 GI:15138034
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 751)
 AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
 TITLE Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer
 JOURNAL Patent: WO 0142467-A 2290 14-JUN-2001;
 Millennium Predictive Medicine, Inc. (US)

FEATURES
 source location/Qualifiers
 1..751
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 194 a 141 c 143 g 269 t 4 others

ORIGIN

Query Match 33.7%; Score 361; DB 6; Length 751;
 Best Local Similarity 100.0%; Pred. No. 8.4e-204;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 712 TGTCCCATCATCTTGTGGGGGAAAAATTTAGTATTTTGAATTTGATCTTACAGC 771
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 DB 684 TGTCCCATCATCTTGTGGGGGAAAAATTTAGTATTTTGAATTTGATCTTACAGC 625
 |||||||
 QY 772 AACAAATAGGAAGTCTGGGCAATGAGAGCTCTTGACAGCATGATCCAGCGATACGA 831
 |||||||
 DB 624 AACAAATAGGAAGTCTGGGCAATGAGAGCTCTTGACAGCATGATCCAGCGATACGA 565
 |||||||
 QY 832 AGCTCTGGCAACAAAATGTGTGGCAATAGATATATCAAGCAATATCTCCACCC 891
 |||||||
 DB 564 AGCTCTGGCAACAAAATGTGTGGCAATAGATATATCAAGCAATATCTCCACCC 505
 |||||||
 QY 892 AAGGCTTGTAAAGTGGGCAATGATATACCTCATAGGGGCTTGTGAGGATTAGATG 951
 |||||||
 DB 504 AAGGCTTGTAAAGTGGGCAATGATATACCTCATAGGGGCTTGTGAGGATTAGATG 445
 |||||||
 QY 952 AATATACCTGTGAAAGTGGGCAATGATATACCTCATAGGGGCTTGTGAGGATTAGATG 1011
 |||||||
 DB 444 AATATACCTGTGAAAGTGGGCAATGATATACCTCATAGGGGCTTGTGAGGATTAGATG 385
 |||||||
 QY 1012 TTTGCATATTAACCAAAATTAATCTGTATCAATAAAACTTGATCCACATGATTT 1071
 |||||||
 DB 384 TTTGCATATTAACCAAAATTAATCTGTATCAATAAAACTTGATCCACATGATTT 325
 |||||||
 QY 1072 C 1072
 |
 DB 324 C 324

RESULT 9
 AX187668/c 468 bp DNA linear PAT 06-AUG-2001
 LOCUS AX187668
 DEFINITION Sequence 3363 from Patent WO0142467.
 ACCESSION AX187668
 VERSION AX187668.1 GI:15139132
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 468)
 AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
 TITLE Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer
 JOURNAL Patent: WO 0142467-A 3363 14-JUN-2001;
 Millennium Predictive Medicine, Inc. (US)

FEATURES
 source location/Qualifiers
 1..468
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 131 a 84 c 94 g 159 t

ORIGIN

Query Match 33.2%; Score 356; DB 6; Length 468;
 Best Local Similarity 100.0%; Pred. No. 7.9e-201;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 CCATATCTTGTGGGGGAAAAATTTAGTATTTTGAATTTGATCTTACAGCAACAA 776
 |||||||
 DB 468 CCATATCTTGTGGGGGAAAAATTTAGTATTTTGAATTTGATCTTACAGCAACAA 409
 |||||||
 QY 777 ATAGGAATCTCTGGGCAATGAGAGCTCTTGACAGCATGATCCAGCGATACGAAGCTC 836
 |||||||
 DB 408 ATAGGAATCTCTGGGCAATGAGAGCTCTTGACAGCATGATCCAGCGATACGAAGCTC 349
 |||||||
 QY 837 TTGCCAACAATAATGTGTGGCAATGAGATATATCAAGCAATATCTCCACCAAGG 896
 |||||||
 DB 348 TTGCCAACAATAATGTGTGGCAATGAGATATATCAAGCAATATCTCCACCAAGG 289
 |||||||
 QY 897 TTCTGTAAAGTGGGCAATGATATACCTCATAGGGGCTTGTGAGGATTAGATGAATA 956
 |||||||
 DB 288 TTCTGTAAAGTGGGCAATGATATACCTCATAGGGGCTTGTGAGGATTAGATGAATA 229
 |||||||
 QY 957 CCTGTAAAGTGGGCAATGATATACCTCATAGGGGCTTGTGAGGATTAGATGAATA 1016
 |||||||
 DB 228 CCTGTAAAGTGGGCAATGATATACCTCATAGGGGCTTGTGAGGATTAGATGAATA 169
 |||||||
 QY 1017 APTTAACCAAAAATTAATCTGTATCAATAAAACTTGATCCACATGATTTTC 1072
 |||||||
 DB 168 APTTAACCAAAAATTAATCTGTATCAATAAAACTTGATCCACATGATTTTC 113
 |||||||

RESULT 10
 AF322456 51381 bp DNA linear HTG 06-DEC-2000
 LOCUS AF322456
 DEFINITION Homo sapiens chromosome 17 clone BAC629B10 map 17p13.3, ***
 SEQUENCING IN PROGRESS ***, 120 unordered pieces.
 ACCESSION AF322456
 VERSION AF322456.1 GI:11559861
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 51381)
 AUTHORS Zhao, X.T., He, M., Wan, D.F., Ye, Y., Qin, W.X., Huang, Y., Zuo, L. and Gu, J.R.
 TITLE Gene clone on human chromosome 17p13.3
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 51381)
 AUTHORS Zhao, X.T., He, M., Wan, D.F., Ye, Y., Qin, W.X., Huang, Y., Zuo, L. and Gu, J.R.
 TITLE Direct Submission
 JOURNAL Submitted (21-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Jun 2200 Xie-Tu Road, Shanghai 200032, P. R. China

COMMENT
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 120 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 236: contig of 236 bp in length
 * 237 435: contig of 199 bp in length
 * 436 665: contig of 230 bp in length
 * 666 879: contig of 214 bp in length
 * 880 1121: contig of 242 bp in length
 * gap of unknown length
 * gap of unknown length
 * gap of unknown length

| | | | | | |
|---|-------|-----------------------------------|---|-------|-----------------------------------|
| * | 1122 | 1948: contig of 827 bp in length | * | 16827 | gap of unknown length |
| * | | gap of unknown length | * | | 17628: contig of 802 bp in length |
| * | 1949 | 2628: contig of 680 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 17629 | 18323: contig of 695 bp in length |
| * | 2629 | 3229: contig of 601 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 18324 | 18532: contig of 209 bp in length |
| * | 3230 | 3893: contig of 664 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 18533 | 18742: contig of 210 bp in length |
| * | 3894 | 4090: contig of 197 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 18743 | 19453: contig of 711 bp in length |
| * | 4091 | 4272: contig of 182 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 19454 | 20109: contig of 656 bp in length |
| * | 4273 | 4420: contig of 148 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 20110 | 20724: contig of 615 bp in length |
| * | 4421 | 4633: contig of 213 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 20725 | 21417: contig of 693 bp in length |
| * | 4634 | 5219: contig of 586 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 21418 | 21679: contig of 262 bp in length |
| * | 5220 | 5881: contig of 662 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 21680 | 21888: contig of 209 bp in length |
| * | 5882 | 6118: contig of 237 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 21889 | 22072: contig of 184 bp in length |
| * | 6119 | 6334: contig of 216 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 22073 | 22788: contig of 716 bp in length |
| * | 6335 | 6484: contig of 150 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 22789 | 23448: contig of 660 bp in length |
| * | 6485 | 6623: contig of 139 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 23449 | 23658: contig of 210 bp in length |
| * | 6624 | 6861: contig of 238 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 23659 | 23869: contig of 211 bp in length |
| * | 6862 | 7067: contig of 206 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 23870 | 24449: contig of 580 bp in length |
| * | 7068 | 7836: contig of 769 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 24450 | 25107: contig of 658 bp in length |
| * | 7837 | 8541: contig of 705 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 25108 | 25316: contig of 209 bp in length |
| * | 8542 | 8731: contig of 190 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 25317 | 25526: contig of 210 bp in length |
| * | 8732 | 8875: contig of 144 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 25527 | 25902: contig of 376 bp in length |
| * | 8876 | 9094: contig of 219 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 25903 | 26555: contig of 653 bp in length |
| * | 9095 | 9684: contig of 590 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 26556 | 26764: contig of 209 bp in length |
| * | 9685 | 10350: contig of 666 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 26765 | 26973: contig of 209 bp in length |
| * | 10351 | 10528: contig of 178 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 26974 | 27587: contig of 614 bp in length |
| * | 10529 | 11128: contig of 600 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 27588 | 27796: contig of 209 bp in length |
| * | 11129 | 11784: contig of 656 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 27797 | 27997: contig of 201 bp in length |
| * | 11785 | 11991: contig of 207 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 27998 | 28229: contig of 237 bp in length |
| * | 11992 | 12648: contig of 657 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 28230 | 28451: contig of 222 bp in length |
| * | 12649 | 13323: contig of 675 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 28452 | 29087: contig of 636 bp in length |
| * | 13324 | 13607: contig of 284 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 29088 | 29741: contig of 654 bp in length |
| * | 13608 | 13833: contig of 226 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 29742 | 29980: contig of 239 bp in length |
| * | 13834 | 14452: contig of 619 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 29981 | 30204: contig of 224 bp in length |
| * | 14453 | 15107: contig of 655 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 30205 | 30725: contig of 521 bp in length |
| * | 15108 | 15743: contig of 636 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 30726 | 31377: contig of 652 bp in length |
| * | 15744 | 16395: contig of 652 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 31378 | 31587: contig of 210 bp in length |
| * | 16396 | 16614: contig of 219 bp in length | * | | gap of unknown length |
| * | | gap of unknown length | * | 31588 | 31792: contig of 205 bp in length |
| * | 16615 | 16826: contig of 212 bp in length | * | | gap of unknown length |

Query Match
Best Local Similarity 14.1% Score 151; DB 2; Length 51381;
Matches 201: Conservative 0; Pred. No. 5.2e-78; Mismatches 1; Indels 0; Gaps 0;

QY 136 GGTGTCGTGAGAACTACCGGATCGGTGTCCTGCTGATGATGCGCAGCAGTGTG 195
|||||
Db 50834 GGTGTCGTGAGAACTACCGGATCGGTGTCCTGCTGATGATGCGCAGCAGTGTG 50893

QY 196 CGGCTTCACAGACACGACTACGAGCCCTGCGACAGCTGACAGACCTGGCCCCCA 255
|||||
Db 50894 CGGCTTCACAGACACGACTACGAGCCCTGCGACAGCTGACAGACCTGGCCCCCA 50953

QY 256 CCACCTCAACGTCGTCCTGTCCTGCAACAGTTGGCCACAGAGCCTGACAGCAA 315
|||||
Db 50954 CCACCTCAACGTCGTCCTGTCCTGCAACAGTTGGCCACAGAGCCTGACAGCAA 51013

QY 316 CAAGGAGATTGAGAGCTTGGCC 337
|||||
Db 51014 CAAGGAGATTGAGAGCTTGGCC 51035

RESULT 11
AF322456 51381 bp DNA linear HTG 06-DEC-2000
LOCUS AF322456/c
DEFINITION Homo sapiens chromosome 17 clone BAC629B10 map 17p13.3, ***
ACCESSION AF322456
VERSION AF322456.1 GI:11559861
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 51381)
Zhao,X.T., He,M., Wan,D.F., Ye,Y., Qin,W.X., Huang,Y., Zuo,L. and
Gu,J.R.
Gene clone on human chromosome 17p13.3
Unpublished
2 (bases 1 to 51381)
Zhao,X.T., He,M., Wan,D.F., Ye,Y., Qin,W.X., Huang,Y., Zuo,L. and
Gu,J.R.
Direct Submission
Submitted (21-NOV-2000) National Laboratory For Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/ln 2200 Xie-Tu Road, Shanghai
200032, P. R. China
* NOTE: This is a 'working draft' sequence. It currently
* consists of 120 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 236: contig of 236 bp in length
* gap of unknown length
* 237 435: contig of 199 bp in length
* gap of unknown length
* 436 665: contig of 230 bp in length

666 gap of unknown length
879: contig of 214 bp in length
gap of unknown length
880 1121: contig of 242 bp in length
gap of unknown length
1122 1948: contig of 827 bp in length
gap of unknown length
1949 2628: contig of 680 bp in length
gap of unknown length
2629 3229: contig of 601 bp in length
gap of unknown length
3230 3893: contig of 664 bp in length
gap of unknown length
3894 4090: contig of 197 bp in length
gap of unknown length
4091 4272: contig of 182 bp in length
gap of unknown length
4273 4420: contig of 148 bp in length
gap of unknown length
4421 4633: contig of 213 bp in length
gap of unknown length
4634 5219: contig of 586 bp in length
gap of unknown length
5220 5881: contig of 662 bp in length
gap of unknown length
5882 6118: contig of 237 bp in length
gap of unknown length
6119 6334: contig of 216 bp in length
gap of unknown length
6335 6484: contig of 150 bp in length
gap of unknown length
6485 6623: contig of 139 bp in length
gap of unknown length
6624 6861: contig of 238 bp in length
gap of unknown length
6862 7067: contig of 206 bp in length
gap of unknown length
7068 7836: contig of 769 bp in length
gap of unknown length
7837 8541: contig of 705 bp in length
gap of unknown length
8542 8731: contig of 190 bp in length
gap of unknown length
8732 8875: contig of 144 bp in length
gap of unknown length
8876 9094: contig of 219 bp in length
gap of unknown length
9095 9684: contig of 590 bp in length
gap of unknown length
9685 10350: contig of 666 bp in length
gap of unknown length
10351 10528: contig of 178 bp in length
gap of unknown length
10529 11128: contig of 600 bp in length
gap of unknown length
11129 11784: contig of 656 bp in length
gap of unknown length
11785 11991: contig of 207 bp in length
gap of unknown length
11992 12648: contig of 657 bp in length
gap of unknown length
12649 13323: contig of 675 bp in length
gap of unknown length
13324 13607: contig of 284 bp in length
gap of unknown length
13608 13833: contig of 226 bp in length
gap of unknown length
13834 14452: contig of 619 bp in length
gap of unknown length
14453 15107: contig of 655 bp in length
gap of unknown length
15108 15743: contig of 636 bp in length
gap of unknown length

* 15744 16395: contig of 652 bp in length
 * 16396 16614: contig of 219 bp in length
 * 16615 16826: contig of 212 bp in length
 * 16827 17628: contig of 802 bp in length
 * 17629 18323: contig of 695 bp in length
 * 18324 18532: contig of 209 bp in length
 * 18533 18742: contig of 210 bp in length
 * 18743 19453: contig of 711 bp in length
 * 19454 20109: contig of 656 bp in length
 * 20110 20724: contig of 615 bp in length
 * 20725 21417: contig of 693 bp in length
 * 21418 21679: contig of 262 bp in length
 * 21680 21888: contig of 209 bp in length
 * 21889 22072: contig of 184 bp in length
 * 22073 22788: contig of 716 bp in length
 * 22789 23448: contig of 660 bp in length
 * 23449 23658: contig of 210 bp in length
 * 23659 23869: contig of 211 bp in length
 * 23870 24449: contig of 580 bp in length
 * 24450 25107: contig of 658 bp in length
 * 25108 25316: contig of 209 bp in length
 * 25317 25526: contig of 210 bp in length
 * 25527 25902: contig of 376 bp in length
 * 25903 26555: contig of 653 bp in length
 * 26556 26764: contig of 209 bp in length
 * 26765 26973: contig of 209 bp in length
 * 26974 27587: contig of 614 bp in length
 * 27588 27796: contig of 209 bp in length
 * 27797 27997: contig of 201 bp in length
 * 27998 28229: contig of 232 bp in length
 * 28230 28451: contig of 222 bp in length
 * 28452 29087: contig of 636 bp in length
 * 29088 29741: contig of 654 bp in length
 * 29742 29980: contig of 239 bp in length
 * 29981 30204: contig of 224 bp in length
 * 30205 30725: contig of 521 bp in length
 * 30726 31377: contig of 652 bp in length

* 31378 31587: contig of 210 bp in length
 * 31588 31792: contig of 205 bp in length
 * 31793 32403: contig of 611 bp in length
 * 32404 33056: contig of 653 bp in length
 * 33057 33266: contig of 210 bp in length
 * 33267 33471: contig of 205 bp in length
 * 33472 34137: contig of 666 bp in length
 * 34138 34789: contig of 652 bp in length
 * 34790 35003: contig of 214 bp in length
 * gap of unknown length

Query Match Best Local Similarity 100.0%; Score 80; DB 2; Length 51381;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 846 AAAATGTGGCAATAGATATCAAGCAATATCTCCACCCAGGCTTGTATAA 905
 Db 49797 AAAATGTGGCAATAGATATCAAGCAATATCTCCACCCAGGCTTGTATAA 49738
 QY 906 CTGGGACCAATGATTCACCTC 925
 Db 49737 CTGGGACCAATGATTCACCTC 49718

RESULT 12
 AC022847/c
 LOCUS
 DEFINITION Homo sapiens chromosome 11 clone RP11-261F7 map 11, LOW-PASS
 SEQUENCE SAMPLING.
 AC022847
 VERSION AC022847.1 GI:6922212
 KEYWORDS HTG; HTGS_PHASE0.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 55891)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens chromosome 11, clone RP11-261F7
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 55891)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barua, N., Beckert, R., Bedalov, F.,
 Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
 Choquel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
 Dearellano, K., Dewar, K., Domingo, M., Doyle, M., Feneator, J.,
 Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
 Garayna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
 Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
 Landers, T., Lehoczek, J., Levine, R., Liu, C., Liu, G., Locke, K.,
 Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,
 McPheters, R., Meldrum, J., Meneses, L., Morrow, J., Naylor, J.,
 Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,
 Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
 Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J.,
 Tirelli, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
 Zimmer, A. and Zody, M.
 DIRECT SUBMISSION
 JOURNAL Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/xk/RepeatMasker.html

```
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6164
Center clone name: 261_F_7

* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1      698: contig of 698 bp in length
*      gap of unknown length
*      699      1436: contig of 738 bp in length
*      gap of unknown length
*      1437      2155: contig of 719 bp in length
*      gap of unknown length
*      2156      2866: contig of 711 bp in length
*      gap of unknown length
*      2867      3559: contig of 693 bp in length
*      gap of unknown length
*      3560      4266: contig of 707 bp in length
*      gap of unknown length
*      4267      4955: contig of 689 bp in length
*      gap of unknown length
*      4956      5656: contig of 701 bp in length
*      gap of unknown length
*      5657      6372: contig of 716 bp in length
*      gap of unknown length
*      6373      7082: contig of 710 bp in length
*      gap of unknown length
*      7083      7807: contig of 725 bp in length
*      gap of unknown length
*      7808      8527: contig of 720 bp in length
*      gap of unknown length
*      8528      9248: contig of 721 bp in length
*      gap of unknown length
*      9249      9953: contig of 705 bp in length
*      gap of unknown length
*      9954      10663: contig of 710 bp in length
*      gap of unknown length
*      10664      11392: contig of 729 bp in length
*      gap of unknown length
*      11393      12092: contig of 700 bp in length
*      gap of unknown length
*      12093      12805: contig of 713 bp in length
*      gap of unknown length
*      12806      13523: contig of 718 bp in length
*      gap of unknown length
*      13524      14261: contig of 738 bp in length
*      gap of unknown length
*      14262      14967: contig of 706 bp in length
*      gap of unknown length
*      14968      15698: contig of 731 bp in length
*      gap of unknown length
*      15699      16427: contig of 729 bp in length
*      gap of unknown length
*      16428      17145: contig of 718 bp in length
*      gap of unknown length
*      17146      17851: contig of 706 bp in length
*      gap of unknown length
*      17852      18565: contig of 714 bp in length
*      gap of unknown length
*      18566      19394: contig of 829 bp in length
*      gap of unknown length

*      19395      20112: gap of unknown length
*      gap of 718 bp in length
*      20113      20839: gap of unknown length
*      gap of 727 bp in length
*      20840      21558: gap of unknown length
*      gap of 719 bp in length
*      21559      22284: gap of unknown length
*      gap of 726 bp in length
*      22285      23015: gap of unknown length
*      gap of 731 bp in length
*      23016      23739: gap of unknown length
*      gap of 724 bp in length
*      23740      24445: gap of unknown length
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*      24446      25157: gap of unknown length
*      gap of 712 bp in length
*      25158      25859: gap of unknown length
*      gap of 702 bp in length
*      25860      26566: gap of unknown length
*      gap of 707 bp in length
*      26567      27276: gap of unknown length
*      gap of 710 bp in length
*      27277      28013: gap of unknown length
*      gap of 737 bp in length
*      28014      28711: gap of unknown length
*      gap of 698 bp in length
*      28712      29426: gap of unknown length
*      gap of 715 bp in length
*      29427      30162: gap of unknown length
*      gap of 736 bp in length
*      30163      30888: gap of unknown length
*      gap of 726 bp in length
*      30889      31586: gap of unknown length
*      gap of 698 bp in length
*      31587      32303: gap of unknown length
*      gap of 717 bp in length
*      32304      33015: gap of unknown length
*      gap of 712 bp in length
*      33016      33733: gap of unknown length
*      gap of 718 bp in length
*      33734      34488: gap of unknown length
*      gap of 735 bp in length
*      34489      35207: gap of unknown length
*      gap of 719 bp in length
*      35208      35929: gap of unknown length
*      gap of 722 bp in length
*      35930      36635: gap of unknown length
*      gap of 706 bp in length
*      36636      37347: gap of unknown length
*      gap of 712 bp in length
*      37348      38065: gap of unknown length
*      gap of 718 bp in length
*      38066      38773: gap of unknown length
*      gap of 708 bp in length
*      38774      39472: gap of unknown length
*      gap of 699 bp in length
*      39473      40189: gap of unknown length
*      gap of 717 bp in length
*      40190      40909: gap of unknown length
*      gap of 720 bp in length
*      40910      41609: gap of unknown length
*      gap of 700 bp in length
*      41610      42332: gap of unknown length
*      gap of 723 bp in length
*      42333      43029: gap of unknown length
*      gap of 697 bp in length
*      43030      43744: gap of unknown length
*      gap of 715 bp in length
*      43745      44481: gap of unknown length
*      gap of 737 bp in length
*      44482      45186: gap of unknown length
*      gap of 705 bp in length
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*      45187      45925: contig of 739 bp in length
*      45926      46640: contig of 715 bp in length
*      46641      47341: contig of 701 bp in length
*      47342      48058: contig of 717 bp in length
*      48059      48769: contig of 711 bp in length
*      48770      49497: contig of 728 bp in length
*      49498      50228: contig of 731 bp in length
*      50229      50941: gap of unknown length
*      50941      gap of 713 bp in length

Query Match
Best Local Similarity 100.0%; Score 79; DB 2; Length 55891;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 TACAGTGTCTCATTCCTCCAGTATTAGCAAGATTGACGCGTACTGTCGCCATCCT 406
      |||
Db 3363 TACAGTGTCTCATTCCTCCAGTATTAGCAAGATTGACGCGTACTGTCGCCATCCT 33574

QY 407 GCCTCAAGTACCTGGGCC 425
      |||
Db 33573 GCCTCAAGTACCTGGGCC 33555

RESULT 13
AX080812      50 bp      DNA      linear      PAT 27-FEB-2001
DEFINITION    AX080812
ACCESSION     AX080812
VERSION       AX080812.1 GI:13169782
KEYWORDS
SOURCE        synthetic construct.
ORGANISM      artificial sequence.
REFERENCE     1 (bases 1 to 50)
AUTHORS       Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
              Kijavyn,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitter,R.M.,
              Matanabe,C.K., and Wood,M.I.
              Method of preventing the injury or death of retinal cells and
              treating ocular diseases
              Patent: WO 0109327-A 58 08-FEB-2001;
              Genentech, Inc. (US)
FEATURES
  source
    1..50
    /organism="synthetic construct"
    /db_xref="taxon:32630"
    /note="Hybridization probe."
BASE COUNT    11 a      12 c      18 g      9 t
ORIGIN

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KEYWORDS
SOURCE        MGC.
ORGANISM      house mouse.
REFERENCE     Mus musculus;
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 1033)
TITLE         Strausberg,R.
JOURNAL       Direct Submission
              Submitted (20-FEB-2001) National Institutes of Health, Mammalian
              Gene Collection (MGC), Cancer Genomics Office, National Cancer
              Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
              USA
REMARK        NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT        Contact: MGC help desk
              Email: gcaps-remail.nih.gov
              Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Baylor College of Medicine Human Genome
              Sequencing Center
              Center code: BCM-HGSC
              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
              Contact: villalona@bcm.tmc.edu.
              Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
              A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
              Muzny,D.M., Gibbs,R.A.
              Clone distribution: MGC clone distribution information can be found
              through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
              Series: IRAC Plate: 6 Row: P Column: 16
              This clone was selected for full length sequencing because it
              passed the following selection criteria: Similarity but not
              identity to protein.
FEATURES
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    1..1033
    /organism="Mus musculus"
    /db_xref="taxon:10090"
    /clone="MGC:6581 IMAGE:3483448"
    /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
    old, gross tissue."
    /clone_1lb="NCI CGAP_Mam5"
    /lab_host="DH10B"
    /note="Vector: pCMV-SPORT6"
    38..598
    /codon_start=1
    /product="Similar to RIKEN CDNA 3110050F08 gene"
    /protein_id="AAH03228.1"
    /db_xref="GI:13096858"
    /translation="MVAATATAMILLMAACAOSRQDFYDKAVINRGKIVLSLEKYG
    VSLVYVNASCGFTDQNYRALQQLQRLDGHHEVLAFPQNGQOQPDNREIENF
    ARRTYSVFPMFSKIAVGTGCAHFAFKLITOTSGKEPTWNVKILVDDPGKVGACMP
    TVPAEIKPRITTEQVMKILRRDEL"
BASE COUNT    264 a      285 c      270 g      214 t
ORIGIN

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Query Match
Best Local Similarity 4.6%; Score 49; DB 10; Length 1033;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 423 CCCAGCTCTGGGAAGAGCCACCTGGAACTTCTGGAAGTACCTAGT 471
      |||
Db 432 CCCAGCTCTGGGAAGAGCCACCTGGAACTTCTGGAAGTACCTAGT 480

RESULT 15
AL627238/C
LOCUS         AL627238      241048 bp      DNA      linear      HTG 31-OCT-2001
DEFINITION    Mus musculus chromosome 4 clone RP23-46M23, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION     AL627238
VERSION       AL627238.6 GI:16580163
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

```

SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (sites)
JOURNAL Direct Submission
Submitted (30-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone
requests: clonerequests@sanger.ac.uk
On Nov 1, 2001 this sequence version replaced gi:16508350.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BM46M23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 23827 bases at least Q40
Consensus quality: 239150 bases at least Q30
Insert size: 239848; sum-of-contigs
Insert size: 228542; 2.6% error; agarose-fp
Quality coverage: 8.48x in Q20 bases; sum-of-contigs Quality
coverage: 10.79x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
source
location/Qualifiers
1. 241048
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
/clone_1lb="RP23-46M23"
1. 2026
/note="assembly_fragment:00289"
2127. 4360
/note="assembly_fragment:05780"
4461. 50623
/note="assembly_fragment:03143"
fragment_chain:1"
50724. 55265
/note="assembly_fragment:04670"
fragment_chain:1"
55366. 57994
/note="assembly_fragment:01496"
fragment_chain:1"
58095. 100479
/note="assembly_fragment:03489"
fragment_chain:1"
100580. 139135
/note="assembly_fragment:01557"
fragment_chain:1"
139236. 158187
/note="assembly_fragment:00668"
fragment_chain:1"
158288. 181745
/note="assembly_fragment:04424"
fragment_chain:1"
181846. 191755
/note="assembly_fragment:00436"
fragment_chain:1"
191856. 196544
/note="assembly_fragment:04437"
fragment_chain:1"
196645. 238408
misc_feature

/note="assembly_fragment:06204"
fragment_chain:1"
238509. 241048
/note="assembly_fragment:02545"
fragment_chain:1"
clone_end:SP6
vector_side:right"
BASE COUNT 66632 a 51150 c 52737 g 69313 t 1216 others
ORIGIN

Query Match 4.3%; Score 46; DB 2; Length 241048;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGACTTCTGGAGAGAGCCACCTGGACTTCTGGAAGTACCTAGT 471
|||||
DB 132611 AGACTTCTGGAGAGAGCCACCTGGAACTTCTGGAAGTACCTAGT 132566

Search completed: August 25, 2002, 07:16:27
Job time: 5781 sec

